



02/18/97

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Rodriguez, Moses  
Miller, David J.  
Asakura, Kunihiro

(ii) TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION  
USING MONOCLONAL AUTOANTIBODIES

(iii) NUMBER OF SEQUENCES: 37

(iv) CORRESPONDENCE ADDRESS:

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Floor  
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(E) COUNTRY: USA  
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/692,084  
(B) FILING DATE: 08-AUG-1996  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/236,520  
(B) FILING DATE: 29-APR-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.  
(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 1199-1-001 CIP

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

08692084-021897

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGGATGGA GATGGATCTT TCTTTTCCTC CTGTCAGGAA CTGCAGGTGT CCATTGCCAG 60  
GTTTCAGCTGC AGCAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCTTTAGT GAAGATATCC 120  
TGCAAGGCTT CTGGTTACAC CTTACAAGC TACGATATAA ACTGGGTGAA GCAGAGGCCT 180  
GGACAGGGAC TTGAGTGGAT TGGATGGATT TATCCTGGAG ATGGTAGTAC TAAGTACAAT 240  
GAGAAATTCA AGGGCAAGGC CACTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 300  
CAGCTCAGCA GCCTGACTTC TGAGAACTCT GCAGTCTATT TCTGTGCAAG AGGGGCCAGG 360  
TTCTACTGGT ACTTCGATGT CTGGGGCGCA GGGACCACGG TCACCGTCTC CTCAGAGAGT 420

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCTGTCT TGGGGCTGCT CTTCTGCCTG GTGACATTCC CAAGCTGTGT CCTATCCCAG 60  
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC 120  
TGCACAGTCT CTGGTTTCTC ATTAAGTAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA 180

GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA	240
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACGCTTCCA AGAGCCAAGT TTTCTTTAAA	300
ATGAACAGTC TGCACGCTAC TGACACAGCC ATATATTATT GTGCCAGAGA CTACGGTAGT	360
AGGGGGGACT ACTGGGGTCA AGGAACCTCA GTCACCGTCT CCTCA	405

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAGTTGT GGTAAACTG GGTTTTTCTT TTAACACTTT TACATGGTAT CCAGTGTGAG	60
GTGAAGCTGG TGGAATCTGG TGGAGGCCTG GTACAGCCTG GGGGTTCTCT GAGACTCTCC	120
TGTGCAACTT CTGGGTTTAC CTTCACTGAT TTCTACATGG AGTGGGTCCG CCAGCCTCCA	180
GGGAAGAGAC TGGAGTGGAT TGCTGCAAGT AGAAAGAAAG CTAATGATTA TAAACAGAG	240
TACAGTGCAT CTGTGAAGGG GCGGTTTACC GTCTCCAGAG ACACTTCCCA AAGCATCCTC	300
TACCTTCAGA TGAATGCCCT GAGAGATGAG GACACTGCCA TTTATTACTG TGCAAGAGAT	360
GCACGGCAGC TCGGGCTCCC GTTTGCTTAC TGGGGCCAAG GGACTCTGGT CACTGTCTCT	420
GCA	423

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

0369204-03499

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGGAATCAC AGACTCTGGT CTTCATATCC ATACTGCTCT GGTATATGG AGCTGATGGG 60  
AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC 120  
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA 180  
GAGCAGTCTC CTAAACTGCT GATATACGGG GCATCCAACC GGTACACTGG GGTCCCCGAT 240  
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTTACTCTGA CCATCAGCAG TGTGCAGGCT 300  
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTACAGCT ATCCGTACAC GTTCCGAGGG 360  
GGGACCAAGC TGGAAATAAA ACGG 384

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGACATGA GGGCTCCTGC ACAGATTTTT GGCTTCTTGT TGCTCTTGTT TCAAGGTACC 60  
AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA 120  
GTCAGTCTCA CTTGTGCGGC AAGTCAGGAC ATTGGTAGTA GCTTAAACTG GCTTCAGCAG 180  
GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTTAGA TTCTGGTGTG 240  
CCCAAAAGGT TCAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAT CAGCAGCCTT 300  
GAGTCTGAAG ATTTTGTAGA CTATTACTGT CTACAATATG CTAGTTCTCC GTACACGTTC 360

GGAGGGGGGA CCAAGCTGGA AATAAACGG GCTGATGCTT CA

402

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGTCAC AGATTCAGGT CTTTGTATTC GTGTTTCTCT GGTGTCTGG TGTGACGGA	60
GACATTGTGA TGACCCAGTC TCACAAATTC ATGTCCACTT CAGTAGGAGA CAGGGTCAGC	120
ATCACCTGCA AGGCCAGTCA GGATGTGAGT ACTGCTGTAG CCTGGTATCA ACAGAAACCA	180
GGACAATCTC CTAAACTACT GATTTACTCG GCATCCTACC GGTACACTGG AGTCCCTGAT	240
CGCTTCACTG GCAGTGGATC TGGGACGGAT TTCACTTTCA CCATCAGCAG TGTGCAGGCT	300
GAAGACCTGG CAGTTTATTA CTGTCAGCAA CATTATACTA CTCCGCTCAC GTTCGGTGCT	360
GGGACCAGGC TGGAGCTGAA ACGGGCTGAT GCTTCA	396

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20250404 18025980



(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGATGGA GATGGATCTT TCTTTTCCTC CTGTCAGGAA CTGCAGGTGT CCATTGCCAG 60  
GTTTCAGCTGC AGCAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCTTTAGT GAAGATATCC 120  
TGCAAGGCTT CTGGTTACAC CTTTACAAGC TACGATATAA ACTGGGTGAA GCAGAGGCCT 180  
GGACAGGGAC TTGAGTGGAT TGGATGGATT TATCCTGGAG ATGGTAGTAC TAAGTACAAT 240  
GAGAAATTCA AGGGCAAGGC CACACTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 300  
CAGCTCAGCA GCCTGACTTC TGAGAACTCT GCAGTCTATT TCTGTGCAAG A 351

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACTGGTACT TCGATGTCTG GGGCGCAGGG ACCACGGTCA CCGTTTCCTC AGAGAGT 57

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

03692094-021897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGCTGTCT TGGGGCTGCT CTTCTGCCTG GTGACATTCC CAAGCGGTGT CCTATCCCAG 60  
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC 120  
TGCACAGTCT CTGGTTTCTC ATTAAGTAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA 180  
GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA 240  
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACAATTCCA AGAGCCAAGT TTTCTTTAAA 300  
ATGAACAGTC TGCAAGCTAA TGACACAGCC ATATATTACT GTGCCAGA 348

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGCTGTCT TAGGGCTGCT CTTCTGCCTA GTGACATTCC CAAGCGGTGT CCTATCCCAG 60  
GTGCAGCTGA AGCAGTCAGG ACCTGGCCTA GTGCAGCCCT CACAGAGCCT GTCCATCACC 120  
TGCACAGTCT CTGGTTTCTC ATTAAGTAGC TATGGTGTAC ACTGGGTTCG CCAGTCTCCA 180  
GGAAAGGGTC TGGAGTGGCT GGGAGTGATA TGGAGTGGTG GAAGCACAGA CTATAATGCA 240  
GCTTTCATAT CCAGACTGAG CATCAGCAAG GACAATTCCA AGAGCCAAGT TTTCTTTAAA 300  
ATGAACAGTC TGCAATCTAA TGACACAGCC ATATATTACT GTGCCAGA 348

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

03692034-02189



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTCCTC A

51

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAAGTTGT GGTAAACTG GGTTTTCTT TTAACACTTT TACATGGTAT CCAGTGTGAG	60
GTGAAGCTGG TGGAATCTGG AGGAGGCTTG GTACAGCCTG GGGGTTCTCT GAGACTCTCC	120
TGTGCAACTT CTGGGTTCAC CTTCAGTGAT TTCTACATGG AGTGGGTCCG CCAGCCTCCA	180
GGGAAGAGAC TGGAGTGGAT TGCTGCAAGT AGAAACAAAG CTAATGATTA TACAACAGAG	240
TACAGTGCAT CTGTGAAGGG TCGGTTTCATC GTCTCCAGAG ACACTTCCCA AAGCATCCTC	300
TACCTTCAGA TGAATGCCCT GAGAGCTGAG GACACTGCCA TTTATTACTG TGCAAGAGAT	360
GCAC	364

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

269204-03189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCTGGTTTG CTTACTGGGG CCAAGGGACT CTGGTCACTG TCTCTGCA

48

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGACATGA GGGCTCCTGC ACAGATTTTT GGCTTCTTGT TGCTCTTGTT TCAAGGTACC 60  
AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA 120  
GTCAGTCTCA CTTGTCGGGC AAGTCAGGAC ATTGGTAGTA GCTTAAACTG GCTTCAGCAG 180  
GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTTAGA TTCTGGTGTG 240  
CCCCAAAGGT TCAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAT CAGCAGCCTT 300  
GAGTCTGAAG ATTTTGTAGA CTATTACTGT CTACAATATG CTAGTTCTCC G 351

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGACATGA GGGCTCCTGC ACAGATTTTT GGCTTCTTGT TGCTCTTGTT TCAAGGTACC 60  
AGATGTGACA TCCAGATGAC CCAGTCTCCA TCCTCCTTAT CTGCCTCTCT GGGAGAAAGA 120

GTCAGTCTCA CTTGTCGGGC AAGTCAGGAC ATTGGTAGTA GCTTAACTG GCTTCAGCAG 180  
 GAACCAGATG GAACTATTAA ACGCCTGATC TACGCCACAT CCAGTTTAGA TTCTGGTGTC 240  
 CCCAAAAGGT TCAGTGGCAG TAGGTCTGGG TCAGATTATT CTCTCACCAT CAGCAGCCTT 300  
 GAGTCTGAAG ATTTTGTAGA CTATTACTGT CTACAATATG CTAGTTCTCC T 351

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TACACGTTTCG GAGGGGGGAC CAAGCTGGAA ATAAAACGGG CTGATGCTTC A 51

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCACGTTTCG GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTTC A 51

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

00692034.024857

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG ATG TCC TCT GCT CAG TTC CTT GGT CTC CTG TTG CTC TGT TTT CAA	48
Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln	
1 5 10 15	
GGT ACC AGA TGT GAT ATC CAG ATG ACA CAG ACT ACA TCC TCC CTG TCT	96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser	
20 25 30	
GCC TCT CTG GGA GAC AGA GTC ACC ATC AGT TGC AGG GCA AGT CAG GAC	144
Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp	
35 40 45	
ATT AGC AAT TAT TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT GTT	192
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val	
50 55 60	
AAA CTC CTG ATC TAC TAC ACA TCA AGA TTA CAC TCA GGA GTC CCA TCA	240
Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser	
65 70 75 80	
AGG TTC AGT GGC AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AGC	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser	
85 90 95	
AAC CTG GAG CAA GAA GAT ATT GCC ACT TAC TTT TGC CAA CAG GGT AAT	336
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn	
100 105 110	
ACG CTT CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG	384
Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg	
115 120 125	
GCT GAT GCT	393

Ala Asp Ala  
130

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln  
1 5 10 15

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser  
20 25 30

Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp  
35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val  
50 55 60

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser  
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser  
85 90 95

Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn  
100 105 110

Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg  
115 120 125

Ala Asp Ala  
130

202504-0439

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATATCCAGA TGACACAGAC TACATCCTCC CTGTCTGCCT CTCTGGGAGA CAGAGTCACC 60  
ATCAGTTGCA GGGCAAGTCA GGACATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA 120  
GATGGAAGTGT TAAACTCCT GATCTACTAC ACATCAAGAT TAACTCAGG AGTCCCATCA 180  
AGGTTCAAGTGCAGTGGGTC TGGAACAGAT TATTCTCTCA CCATTAGCAA CCTGGAGCAA 240  
GAAGATATTG CCACTTACTT TTGCCAACAG GGAATACGC TTCCTCCGAC GTTCGGTGGA 300  
GGCACCAAGC TGGAAATCAA ACGG 324

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATATCCAGA TGACACAGAC TACATCCTCC CTGTCTGCCT CTCTGGGAGA CAGAGTCACC 60  
ATCAGTTGCA GGGCAAGTCA GGACATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA 120  
GATGGAAGTGT TAAACTCCT GATCTACTAC ACATCAAGAT TAACTCAGG AGTCCCATCA 180

AGGTTTCAGTG GCAGTGGGTC TGGAACAGAT TATTCTCTCA CCATTAGCAA CCTGGAGCAA 240

GAAGATATTG CCACTTACTT TTGCCAACAG GGTAATACGC TTCCT 285

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGACGTTTCG GTGGAGGCAC CAAGCTGGAA ATCAAACGT 39

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 429 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG GGA TGG AGC TGT ATC ATC CTC TTT TTG GTA GCA GCA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
1 5 10 15

GTC CAC TCC CAG GTC CAA CTG CAG CAG CCT GGG ACT GAA CTG GTG AAG 96  
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys  
20 25 30

CCT GGG GCT TCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC ACC TTC 144

069044.039

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

ACC AGC TAC TGG ATG CAC TGG GTG AAG CAG AGG CCT GGA CAA GGC CTT 192  
 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
 50 55 60

GAG TGG ATT GGA AAT ATT AAT CCT AGC AAT GGT GGT ACT AAC TAC AAT 240  
 Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn  
 65 70 75 80

GAG AAG TTC AAG AGC AAG GCC ACA CTG ACT GTA GAC AAA TCC TCC AGC 288  
 Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser  
 85 90 95

ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC 336  
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
 100 105 110

TAT TAT TAT GCA AGA CGG GCC CCT TAC TAC GGT AGT AGG AAC TTT GAC 384  
 Tyr Tyr Tyr Ala Arg Arg Ala Pro Tyr Tyr Gly Ser Arg Asn Phe Asp  
 115 120 125

TAC TGG GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA GAG AGT CAG 429  
 Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Gln  
 130 135 140

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly  
 1 5 10 15

CC026980-402616



Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys  
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser  
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
100 105 110

Tyr Tyr Tyr Ala Arg Arg Ala Pro Tyr Tyr Gly Ser Arg Asn Phe Asp  
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Glu Ser Gln  
130 135 140

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAG GTC CAA CTG CAG CAG CCT GGG ACT GAA CTG GTG AAG CCT GGG GCT  
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

TCA GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC ACC TTC ACC AGC TAC 96  
 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
                   20                  25                  30

TGG ATG CAC TGG GTG AAG CAG AGG CCT GGA CAA GGC CTT GAG TGG ATT 144  
 Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
                   35                  40                  45

GGA AAT ATT AAT CCT AGC AAT GGT GGT ACT AAC TAC AAT GAG AAG TTC 192  
 Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
                   50                  55                  60

AAG AGC AAG GCC ACA CTG ACT GTA GAC AAA TCC TCC AGC ACA GCC TAC 240  
 Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
                   65                  70                  75                  80

ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAT TAT 288  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr  
                                   85                  90                  95

GCA AGA GAT TAC TAC GGT AGT AGC TGG GGG TAC TAC TTT GAC TAC TGG 336  
 Ala Arg Asp Tyr Tyr Gly Ser Ser Trp Gly Tyr Tyr Phe Asp Tyr Trp  
                   100                  105                  110

GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA 366  
 Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
                   115                  120

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala  
           1                  5                  10                  15

0869204-0169

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Tyr  
85 90 95

Ala Arg Asp Tyr Tyr Gly Ser Ser Trp Gly Tyr Tyr Phe Asp Tyr Trp  
100 105 110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGGGATGGA GCTGTATCAT CCTCTTTTGT GTAGCAGCAG CTACAGGTGT CCACTCCCAG	60
GTCCAAGTGC AGCAGCCTGG GACTGAACTG GTGAAGCCTG GGGCTTCAGT GAAGCTGTCC	120
TGCAAGGCTT CTGGCTACAC CTTCAACCAGC TACTGGATGC ACTGGGTGAA GCAGAGGCCT	180
GGACAAGGCC TTGAGTGGAT TGGAAATATT AATCCTAGCA ATGGTGGTAC TAACTACAAT	240

08692084-021397

GAGAAGTTCA AGAGCAAGGC CACACTGACT GTAGACAAAT CCTCCAGCAC AGCCTACATG 300

CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ATTATGCAAG A 351

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TACTTTGACT ACTGGGGCCA AGGCACCACT CTCACAGTCT CCTCA 45

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Gly	Trp	Arg	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Ala	Gly
1				5					10					15	

Val	His	Cys	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys
			20					25					30		

Pro	Gly	Ala	Leu	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

Thr	Ser	Tyr	Asp	Ile	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu
	50						55				60				

Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn  
 65 70 75 80  
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95  
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val  
 100 105 110  
 Tyr Phe Cys Ala Arg Gly Ala Arg Phe Tyr Trp Tyr Phe Asp Val Trp  
 115 120 125  
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser  
 130 135

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys  
 1 5 10 15  
 Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln  
 20 25 30  
 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu  
 35 40 45  
 Thr Ser Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala  
 65 70 75 80  
 Ala Phe Ile Ser Arg Leu Ser Ile Ser Lys Asp Ala Ser Lys Ser Gln  
 85 90 95

03692084-021897



Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
 130 135 140

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Glu	Ser	Gln	Thr	Leu	Val	Phe	Ile	Ser	Ile	Leu	Leu	Trp	Leu	Tyr	1	5	10	15
Gly	Ala	Asp	Gly	Asn	Ile	Val	Met	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ser	20	25	30	
Met	Ser	Val	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys	Ala	Ser	Glu	Asn	35	40	45	
Val	Val	Thr	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Gln	Ser	Pro	50	55	60	
Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	65	70	75	80
Arg	Phe	Thr	Gly	Ser	Gly	Ser	Ala	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	85	90	95	
Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Gly	Tyr	100	105	110	
Ser	Tyr	Pro	Tyr	Thr	Phe	Arg	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	115	120	125	

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

00662004-0306980

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Asp Met Arg Ala Pro Ala Gln Ile Phe Gly Phe Leu Leu Leu Leu  
1 5 10 15  
Phe Gln Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30  
Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser  
35 40 45  
Gln Asp Ile Gly Ser Ser Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly  
50 55 60  
Thr Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val  
65 70 75 80  
Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr  
85 90 95  
Ile Ser Ser Leu Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln  
100 105 110  
Tyr Ala Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile  
115 120 125  
Lys Arg  
130

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

08592084-031897



(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Glu Ser Gln Ile Gln Val Phe Val Phe Val Phe Leu Trp Leu Ser  
1                      5                      10                      15  
Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser  
                    20                      25                      30  
Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp  
                    35                      40                      45  
Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro  
                    50                      55                      60  
Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp  
65                      70                      75                      80  
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser  
                    85                      90                      95  
Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr  
                    100                      105                      110  
Thr Thr Pro Leu Thr Phe Gly Ala Gly Thr Arg Leu Glu Leu Lys Arg  
                    115                      120                      125

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

0069204 02189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys  
1 5 10 15  
Val Leu Ser Gln Val Gln Leu Arg Gln Ser Gly Pro Gly Leu Val Gln  
20 25 30  
Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu  
35 40 45  
Thr Ser Tyr Gly Val His Trp Phe Arg Gln Ser Pro Gly Lys Gly Leu  
50 55 60  
Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala  
65 70 75 80  
Ala Phe Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln  
85 90 95  
Val Phe Phe Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr  
100 105 110  
Tyr Cys Ala Arg Asn Arg Gly Arg Tyr Asn Tyr Tyr Ala Met Asp Tyr  
115 120 125  
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
130 135

268120-48026980